

SEQUENCE LISTING

<110> Sheppard, Paul O.
 Baindur, Nand
 Deisher, Theresa A.
 Bishop, Paul D.

<120> DISINTEGRIN HOMOLOG

<130> 98-29

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<210> 1

<211> 2268

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)...(2090)

<221> misc_feature

<222> (1)...(2268)

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cag caa aaa cat aat aag gct gtc cat ctg gcc cag gca agc ttc cag	95
Gln Gln Lys His Asn Lys Ala Val His Leu Ala Gln Ala Ser Phe Gln	
20 25 30	

att gaa gcc ttc ggc tcc aaa ttc att ctt gac ctc ata ctg aac aat	143
Ile Glu Ala Phe Gly Ser Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn	
35 40 45	

ggt ttg ttg tct tct gat tat gtg gag att cac tac gaa aat ggg aaa	191
Gly Leu Leu Ser Ser Asp Tyr Val Glu Ile His Tyr Glu Asn Gly Lys	
50 55 60	

cca	cag	tac	tct	aag	ggt	gga	gag	cac	tgt	tac	tac	cat	gga	agc	atc	239
Pro	Gln	Tyr	Ser	Lys	Gly	Gly	Glu	His	Cys	Tyr	Tyr	His	Gly	Ser	Ile	
	65					70					75					
aga	ggc	gtc	aaa	gac	tcc	aag	gtg	gct	ctg	tca	acc	tgc	aat	gga	ctt	287
Arg	Gly	Val	Lys	Asp	Ser	Lys	Val	Ala	Leu	Ser	Thr	Cys	Asn	Gly	Leu	
	80				85				90						95	
cat	ggc	atg	ttt	gaa	gat	gat	acc	ttc	gtg	tat	atg	ata	gag	cca	cta	335
His	Gly	Met	Phe	Glu	Asp	Asp	Thr	Phe	Val	Tyr	Met	Ile	Glu	Pro	Leu	
				100					105					110		
gag	ctg	gtt	cat	gat	gag	aaa	agc	aca	ggt	cga	cca	cat	ata	atc	cag	383
Glu	Leu	Val	His	Asp	Glu	Lys	Ser	Thr	Gly	Arg	Pro	His	Ile	Ile	Gln	
			115					120					125			
aaa	acc	ttg	gca	gga	cag	tat	tct	aag	caa	atg	aag	aat	ctc	act	atg	431
Lys	Thr	Leu	Ala	Gly	Gln	Tyr	Ser	Lys	Gln	Met	Lys	Asn	Leu	Thr	Met	
		130					135					140				
gaa	aga	ggt	gac	cag	tgg	ccc	ttt	ctc	tct	gaa	tta	cag	tgg	ttg	aaa	479
Glu	Arg	Gly	Asp	Gln	Trp	Pro	Phe	Leu	Ser	Glu	Leu	Gln	Trp	Leu	Lys	
	145					150					155					
aga	agg	aag	aga	gca	gtg	aat	cca	tca	cgt	ggt	ata	ttt	gaa	gaa	atg	527
Arg	Arg	Lys	Arg	Ala	Val	Asn	Pro	Ser	Arg	Gly	Ile	Phe	Glu	Glu	Met	
	160				165					170					175	
aaa	tat	ttg	gaa	ctt	atg	att	ggt	aat	gat	cac	aaa	acg	tat	aag	aag	575
Lys	Tyr	Leu	Glu	Leu	Met	Ile	Gly	Asn	Asp	His	Lys	Thr	Tyr	Lys	Lys	
				180					185					190		
cat	cgc	tct	tct	cat	gca	cat	acc	aac	aac	ttt	gca	aag	tcc	gtg	gtc	623
His	Arg	Ser	Ser	His	Ala	His	Thr	Asn	Asn	Phe	Ala	Lys	Ser	Val	Val	
				195				200					205			
aac	ctt	gtg	gat	tct	att	tac	aag	gag	cag	ctc	aac	acc	agg	gtt	gtc	671
Asn	Leu	Val	Asp	Ser	Ile	Tyr	Lys	Glu	Gln	Leu	Asn	Thr	Arg	Val	Val	
		210					215					220				
ctg	gtg	gct	gta	gag	acc	tgg	act	gag	aag	gat	cag	att	gac	atc	acc	719
Leu	Val	Ala	Val	Glu	Thr	Trp	Thr	Glu	Lys	Asp	Gln	Ile	Asp	Ile	Thr	
	225					230					235					

acc aac cct gtg cag atg ctc cat gag ttc tca aaa tac cgg cag cgc	767
Thr Asn Pro Val Gln Met Leu His Glu Phe Ser Lys Tyr Arg Gln Arg	
240 245 250 255	
att aag cag cat gct gat gct gtg cac ctc atc tcg cgg gtg aca ttt	815
Ile Lys Gln His Ala Asp Ala Val His Leu Ile Ser Arg Val Thr Phe	
260 265 270	
cac tat aag aga agc agt ctg agt tac ttt gaa ggt gtc tgt tct cgc	863
His Tyr Lys Arg Ser Ser Leu Ser Tyr Phe Glu Gly Val Cys Ser Arg	
275 280 285	
aca aga gga gtt ggt gtg aat gag tat ggt ctt cca atg gca gtg gca	911
Thr Arg Gly Val Gly Val Asn Glu Tyr Gly Leu Pro Met Ala Val Ala	
290 295 300	
caa gta tta tcg cag agc ctg gct caa aac ctt gga atc caa tgg gaa	959
Gln Val Leu Ser Gln Ser Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu	
305 310 315	
cct tct agc aga aag cca aaa tgt gac tgc aca gaa tcc tgg ggt ggc	1007
Pro Ser Ser Arg Lys Pro Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly	
320 325 330 335	
tgc atc atg gag gaa aca ggg gtg tcc cat tct cga aaa ttt tca aag	1055
Cys Ile Met Glu Glu Thr Gly Val Ser His Ser Arg Lys Phe Ser Lys	
340 345 350	
tgc agc att ttg gag tat aga gac ttt tta cag aga gga ggt gga gcc	1103
Cys Ser Ile Leu Glu Tyr Arg Asp Phe Leu Gln Arg Gly Gly Gly Ala	
355 360 365	
tgc ctt ttc aac agg cca aca aag cta ttt gag ccc acg gaa tgt gga	1151
Cys Leu Phe Asn Arg Pro Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly	
370 375 380	
aat gga tac gtg gaa gct ggg gag gag tgt gat tgt ggt ttt cat gtg	1199
Asn Gly Tyr Val Glu Ala Gly Glu Glu Cys Asp Cys Gly Phe His Val	
385 390 395	
gaa tgc tat gga tta tgc tgt aag aaa tgt tcc ctc tcc aac ggg gct	1247
Glu Cys Tyr Gly Leu Cys Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala	
400 405 410 415	

cac tgc agc gac ggg ccc tgc tgt aac aat acc tca tgt ctt ttt cag	1295
His Cys Ser Asp Gly Pro Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln	
420 425 430	
cca cga ggg tat gaa tgc cgg gat gct gtg aac gag tgt gat att act	1343
Pro Arg Gly Tyr Glu Cys Arg Asp Ala Val Asn Glu Cys Asp Ile Thr	
435 440 445	
gaa tat tgt act gga gac tct ggt cag tgc cca cca aat ctt cat aag	1391
Glu Tyr Cys Thr Gly Asp Ser Gly Gln Cys Pro Pro Asn Leu His Lys	
450 455 460	
caa gac gga tat gca tgc aat caa aat cag ggc egc tgc tac aat ggc	1439
Gln Asp Gly Tyr Ala Cys Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly	
465 470 475	
gag tgc aag acc aga gac aac cag tgt cag tac atc tgg gga aca aag	1487
Glu Cys Lys Thr Arg Asp Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys	
480 485 490 495	
gct gca ggg tct gac aag ttc tgc tat gaa aag ctg aat aca gaa ggc	1535
Ala Ala Gly Ser Asp Lys Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly	
500 505 510	
act gag aag gga aac tgc ggg aag gat gga gac cgg tgg att cag tgc	1583
Thr Glu Lys Gly Asn Cys Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys	
515 520 525	
agc aaa cat gat gtg ttc tgt gga ttc tta ctc tgt acc aat ctt act	1631
Ser Lys His Asp Val Phe Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr	
530 535 540	
cga gct cca cgt att ggt caa ctt cag ggt gag atc att cca act tcc	1679
Arg Ala Pro Arg Ile Gly Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser	
545 550 555	
ttc tac cat caa ggc cgg gtg att gac tgc agt ggt gcc cat gta gtt	1727
Phe Tyr His Gln Gly Arg Val Ile Asp Cys Ser Gly Ala His Val Val	
560 565 570 575	
tta gat gat gat acg gat gtg ggc tat gta gaa gat gga acg cca tgt	1775
Leu Asp Asp Asp Thr Asp Val Gly Tyr Val Glu Asp Gly Thr Pro Cys	
580 585 590	

ggc ccg tct atg atg tgt tta gat cgg aag tgc cta caa att caa gcc 1823
 Gly Pro Ser Met Met Cys Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala
 595 600 605

cta aat atg agc agc tgt cca ctc gat tcc aag ggt aaa gtc tgt tcg 1871
 Leu Asn Met Ser Ser Cys Pro Leu Asp Ser Lys Gly Lys Val Cys Ser
 610 615 620

ggc cat ggg gtg tgt agt aat gaa gcc acc tgc att tgt gat ttc acc 1919
 Gly His Gly Val Cys Ser Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr
 625 630 635

tgg gca ggg aca gat tgc agt atc cgg gat cca gtt agg aac ctt cac 1967
 Trp Ala Gly Thr Asp Cys Ser Ile Arg Asp Pro Val Arg Asn Leu His
 640 645 650 655

ccc ccc aag gat gaa gga ccc aag ggt ttg tgt gat ttt ggt ttc aat 2015
 Pro Pro Lys Asp Glu Gly Pro Lys Gly Leu Cys Asp Phe Gly Phe Asn
 660 665 670

tca tgg aat act gaa ttc gtt gac act gtt cca atg cac cag tat aac 2063
 Ser Trp Asn Thr Glu Phe Val Asp Thr Val Pro Met His Gln Tyr Asn
 675 680 685

att cta att gac tta aga gga gac aca taagaatatc ngtttttgcc 2110
 Ile Leu Ile Asp Leu Arg Gly Asp Thr
 690 695

tttaaagtat ataatttatg ttactgccaa attaaggatt ctgatatatc atatttttaa 2170
 aatgtgtttg aattacttct tagtctagaa ctgagattgg gaagaagtaa atatacacat 2230
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<212> PRT

<213> Homo sapiens

<400> 2

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 20 25 30
 Glu Ala Phe Gly Ser Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly
 35 40 45

Leu Leu Ser Ser Asp Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro
 50 55 60
 Gln Tyr Ser Lys Gly Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg
 65 70 75 80
 Gly Val Lys Asp Ser Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His
 85 90 95
 Gly Met Phe Glu Asp Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu
 100 105 110
 Leu Val His Asp Glu Lys Ser Thr Gly Arg Pro His Ile Ile Gln Lys
 115 120 125
 Thr Leu Ala Gly Gln Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu
 130 135 140
 Arg Gly Asp Gln Trp Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg
 145 150 155 160
 Arg Lys Arg Ala Val Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys
 165 170 175
 Tyr Leu Glu Leu Met Ile Gly Asn Asp His Lys Thr Tyr Lys Lys His
 180 185 190
 Arg Ser Ser His Ala His Thr Asn Asn Phe Ala Lys Ser Val Val Asn
 195 200 205
 Leu Val Asp Ser Ile Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu
 210 215 220
 Val Ala Val Glu Thr Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr
 225 230 235 240
 Asn Pro Val Gln Met Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile
 245 250 255
 Lys Gln His Ala Asp Ala Val His Leu Ile Ser Arg Val Thr Phe His
 260 265 270
 Tyr Lys Arg Ser Ser Leu Ser Tyr Phe Glu Gly Val Cys Ser Arg Thr
 275 280 285
 Arg Gly Val Gly Val Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln
 290 295 300
 Val Leu Ser Gln Ser Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro
 305 310 315 320
 Ser Ser Arg Lys Pro Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys
 325 330 335
 Ile Met Glu Glu Thr Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys
 340 345 350
 Ser Ile Leu Glu Tyr Arg Asp Phe Leu Gln Arg Gly Gly Gly Ala Cys
 355 360 365
 Leu Phe Asn Arg Pro Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn
 370 375 380
 Gly Tyr Val Glu Ala Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu
 385 390 395 400

Cys Tyr Gly Leu Cys Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala His
 405 410 415
 Cys Ser Asp Gly Pro Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro
 420 425 430
 Arg Gly Tyr Glu Cys Arg Asp Ala Val Asn (Glu Cys Asp) Ile Thr Glu
 435 440 445
 Tyr Cys Thr Gly Asp Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln
 450 455 460
 Asp Gly Tyr Ala Cys Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu
 465 470 475 480
 Cys Lys Thr Arg Asp Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala
 485 490 495
 Ala Gly Ser Asp Lys Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr
 500 505 510
 Glu Lys Gly Asn Cys Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser
 515 520 525
 Lys His Asp Val Phe Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg
 530 535 540
 Ala Pro Arg Ile Gly Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe
 545 550 555 560
 Tyr His Gln Gly Arg Val Ile Asp Cys Ser Gly Ala His Val Val Leu
 565 570 575
 Asp Asp Asp Thr Asp Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly
 580 585 590
 Pro Ser Met Met Cys Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu
 595 600 605
 Asn Met Ser Ser Cys Pro Leu Asp Ser Lys Gly Lys Val Cys Ser Gly
 610 615 620
 His Gly Val Cys Ser Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr Trp
 625 630 635 640
 Ala Gly Thr Asp Cys Ser Ile Arg Asp Pro Val Arg Asn Leu His Pro
 645 650 655
 Pro Lys Asp Glu Gly Pro Lys Gly Leu Cys Asp Phe Gly Phe Asn Ser
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 690 695

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<211> 2088

<212> DNA

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<221> variation

<222> (1)...(2088)

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<223> n = A,T,C or G

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ytngayytna	thytnaayaa	yggnytnytn	wsnwsngayt	aygtngarat	hcaytaygar	180
aayggnaarc	cncartayws	naargggngn	garcaytgyt	aytaycaygg	nwsnathmgn	240
ggngtnaarg	aywsnaargt	ngcnytnwsn	acntgyaayg	gnytncaayg	natgttygar	300
gaygayacnt	tygtntayat	gathgarccn	ytngarytng	tncaygayga	raarwsnacn	360
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mgnaarmgng	cngtnaaycc	nwsnmngngn	athhttygarg	aratgaarta	yytngarytn	540
atgathggna	aygaycayaa	racntayaar	aarcaymgng	snwsncaygc	ncayacnaay	600
aayttygcna	arwsngtngt	naayytngtn	gaywsnatht	ayaargarca	rytnaayacn	660
mgngtngtny	tngtngcngt	ngaracntgg	acngaraarg	aycarathga	yathacnacn	720
aayccngtnc	aratgytnca	ygarttywsn	aartaymgnc	armgnathaa	rcarcaygc	780
gaygcngtnc	ayytnathws	nmngngtnacn	ttycaytaya	armgnwsnws	nytnwsntay	840
ttygarggng	tntgywsnmg	nacnmngngn	gtnggngtna	aygartaygg	nytnccnatg	900
gcngtngcnc	argtnytnws	ncarwsnytn	gcncaraayy	tnggnathca	rtgggarccn	960
wsnwsnmgna	arccnaartg	ygaytgyacn	garwsntggg	ngngntgyat	hatggargar	1020
acnggngtnw	sncaywsnmg	naarttywsn	aartgywsna	thytngarta	ymnggaytty	1080
ytncaarmgng	gnggnggngc	ntgyytntty	aaymgncna	cnaarytntt	ygarccnacn	1140
gartgyggna	ayggntaygt	ngargcnggn	gargartgyg	aytgyggntt	ycaygtngar	1200
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ytncayaarc	argayggnta	ygcntgyaay	caraaycarg	gnmgntgyta	yaayggngar	1440
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aarttytgyt	aygaraaryt	naayacngar	ggnacngara	arggnaaytg	yggnaargay	1560
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aayytnacnm	gngcnccnmg	nathggncar	ytnarggng	arathathcc	nacnwsntty	1680
taycaycarg	gnmgngtnat	hgaytgywsn	gngcncayg	tngtnytnga	ygaygayacn	1740
gaygtnggnt	aygtngarga	yggnacccn	tgyggncnw	snatgatgtg	yytngaymgn	1800
aartgyytnc	arathcargc	nytnaayatg	wsnwsntgyc	cnytngayws	naarggnaar	1860
gtntgywsng	gncayggngt	ntgywsnaay	gargcnacnt	gyathtgyga	ytyyacntgg	1920
gcnggnacng	aytgywsnat	hmgngayccn	gtnmgnaayy	tncayccncc	naargaygar	1980
ggncncaarg	gnytnntgyga	ytytgngntty	aaywsntgga	ayacngartt	ygtngayacn	2040

gtnccnatgc aycartayaa yathytnath gayytnmgng gngayacn

2088

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<212> DNA

<213> Artificial Sequence

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23

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<212> DNA

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<223> oligonucleotide ZC17992

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23

<210> 6

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<212> DNA

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<212> PRT

<213> Artificial Sequence

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Lys Arg Arg Lys Arg Ala
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Leu Lys Arg Arg Lys Arg
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Lys Lys His Arg Ser Ser
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<210> 12

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<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide primer ZC20.844

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18